

Appl. No. 09/825,212  
Arndt. dated August 25, 2005  
Reply to Office Action of May 25, 2005

AMENDMENTS TO THE CLAIMS

Amendments to the Claims:

Please amend the claims as follows:

Listing of Claims:

This Listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-46 (Cancelled)

Claim 47 (Currently Amended) A method for crystallizing *S. aureus* thioredoxin reductase comprising:

Preparing purified *S. aureus* thioredoxin reductase at a concentration of about 1mg/ml to about 50mg/ml, wherein the amino acid sequence of the *S. aureus* thioredoxin reductase comprises SEQ IE NO:1, or SEQ ID NO:1, except that at least one methionine is replaced with selenomethionine; and

Crystallizing *S. aureus* thioredoxin reductase (SEQ ID NO:1) from a solution at a pH of about 6 to about 10 and comprising about 0 wt. % to about 40 wt. % DMSO and about 100 mM to about 6 M sodium formate.

Claim 48 (Currently Amended) A crystal of *S. aureus* thioredoxin reductase (SEQ ID NO:1).

Claim 49 (Original) The crystal of claim 48 having the tetragonal space group symmetry P4<sub>3</sub>2<sub>1</sub>2.

Claim 50 (Original) The crystal of claim 48 comprising a unit cell having dimensions a, b, and c; wherein a is about 70Å to about 110 Å, b is about 70Å to about 110Å, c is about 160Å to about 220Å, and  $\alpha=\beta=\gamma=90^\circ$ .

Claim 51 (Original) The crystal of claim 48 comprising atoms arranged in a spatial relationship represented by the structure coordinates listed in Table 1.

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Claim 52 (Currently Amended) A crystal of *S. aureus* thioredoxin reductase (SEQ ID NO:1) wherein the thioredoxin reductase has amino acid sequence SEQ ID NO:1.

Claim 53 (Currently Amended) A crystal of *S. aureus* thioredoxin reductase (SEQ ID NO:1) wherein the thioredoxin reductase has amino acid sequence SEQ ID NO:1, except that at least one methionine is replaced with selenomethionine.

Claim 54 (Currently Amended) A crystal of *S. aureus* thioredoxin reductase (SEQ ID NO:1) having tetragonal space group symmetry P4<sub>3</sub>2<sub>1</sub>2 and comprising a unit cell having dimensions a, b, and c; wherein a is about 70Å to about 110 Å, b is about 70Å to about 110Å, c is about 160Å to about 220Å, and  $\alpha=\beta=\gamma=90^\circ$ .

55. (Currently Amended) A polypeptide consisting of a portion of *S. aureus* thioredoxin reductase (SEQ ID NO:1) starting at one of amino acids 10 to 12 and ending at one of amino acids 290 to 297 of *S. aureus* thioredoxin reductase as set forth in SEQ ID NO: 1.

56. (Previously Presented) The polypeptide of claim 55, wherein the three-dimensional configuration of the amino acids listed in Table 2, is defined by a set of points having a root mean square deviation of less than about 1.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

57. (Previously Presented) The polypeptide of claim 55, wherein the three-dimensional configuration of the amino acids listed in Table 3, is defined by a set of points having a root mean square deviation of less than about 1.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

58. (Previously Presented) The polypeptide of claim 55, wherein the three-dimensional configuration of the amino acids listed in Table 4, is defined by a set of points having a root mean square deviation of less than about 1.1 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

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59. (Currently Amended) A polypeptide consisting of a portion of *S. aureus* thioredoxin reductase (SEQ ID NO:1) starting at one of amino acids 43 to 52 and ending at one of amino acids 286 to 289 of *S. aureus* thioredoxin reductase as set forth in SEQ ID NO: I.

60. (Previously Presented) The polypeptide of claim 59, wherein the three-dimensional configuration of Cys 135, Cys 138, and the amino acids listed in Table 5, is defined by a set of points having a root mean square deviation of less than about 0.8 from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

61. (Previously Presented) The polypeptide of claim 59, wherein the three-dimensional configuration of Cys 135, Cys 138, and the amino acids listed in Table 6, is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.

62. (Previously Presented) The polypeptide of claim 59, wherein the three-dimensional configuration of Cys 135, Cys 138, and the amino acids listed in Table 7, is defined by a set of points having a root mean square deviation of less than about 0.8 Å from points representing the backbone atoms of said amino acids as represented by structure coordinates listed in Table 1.